

	M	A	S	L	D	R	V	K	V	L	V	L	G	D	S	SEQ ID NO:2				
AGGGAAAGCCAGTGGCAAG	ATG	CGG	TCC	CTG	GAT	CGG	GTG	AAG	GTA	CTG	GTG	TTG	GGA	GAC	TCA	SEQ ID NO:1				
↑SEQ ID NO:3→																				
G	V	G	K	S	S	L	V	H	L	L	C	Q	N	Q	V	35				
GGT	GTT	GGG	AAA	TCT	TCG	TTA	GTC	CAT	CTC	CTA	TGC	CAA	AAT	CAA	GTG	CTG	GGA	AAT	CCA	105
S	W	T	V	G	C	S	V	D	V	R	V	H	D	Y	K	E	G	T	P	55
TCA	TGG	ACT	GTG	GGC	TGC	TCA	GTG	GAT	GTC	AGA	GTT	CAT	GAT	TAC	AAA	GAA	GGA	ACC	CCA	165
E	E	K	T	Y	Y	E	E	L	W	D	V	G	G	S	V	G	S	A	S	75
GAA	GAG	AAG	ACC	TAC	TAC	ACA	GAA	TTA	TGG	GAT	GTT	GGG	GCG	TCT	GTG	GGC	AGT	GCC	AGC	225
S	V	K	S	T	R	A	V	F	Y	N	S	V	N	G	I	I	F	V	H	95
AGC	GTG	AAA	AGC	ACA	AGA	GCA	GTA	TTC	TAC	AAC	TCC	GTA	AAT	GGT	ATT	ATT	TTC	GTA	CAC	285
D	L	T	N	K	K	S	S	Q	N	L	R	R	W	S	L	E	A	L	N	115
GAC	TTA	ACA	AAT	AAG	AAG	TCC	TCC	CAA	AAC	TTG	CGT	CGT	TGG	TCA	TTG	GAA	GCT	CTC	AAC	345
R	D	L	V	P	T	G	V	L	V	T	N	G	D	Y	D	Q	E	Q	F	135
AGG	GAT	TTG	GTG	CCA	ACT	GGA	GTC	TTG	GTG	ACA	AAT	GGG	GAT	TAT	GAT	CAA	GAA	CAG	TTT	405
A	D	N	Q	I	P	L	L	V	I	G	T	K	L	D	Q	I	H	E	T	155
GCT	GAT	AAC	CAA	ATA	CCA	CTG	TTG	GTA	ATA	GGG	ACT	AAA	CTG	GAC	CAG	ATT	CAT	GAA	ACA	465
K	R	H	E	V	L	T	R	T	A	F	L	A	E	D	F	N	P	E	E	175
AAG	CGC	CAT	GAA	GTT	TTA	ACT	AGG	ACT	GCT	TTC	CTG	GCT	GAG	GAT	TTC	ATT	CCA	GAA	GAA	525
I	N	L	D	C	T	N	P	R	Y	L	A	A	G	S	S	N	A	V	K	195
ATT	AAT	TTG	GAC	TGC	ACA	AAT	CCA	CGG	TAC	TTA	GCT	GCA	GGT	TCT	TCC	ATT	GCT	GTC	AAG	585
L	S	R	F	F	D	K	V	I	E	K	R	Y	F	L	R	E	G	N	Q	215
CTC	AGT	AGG	TTT	TTT	GAT	AGG	GTC	ATA	GAG	AAG	AGA	TAC	TTT	TTA	AGA	GAA	GGT	ATT	CAG	645
I	P	G	F	P	D	R	K	R	F	G	A	G	T	L	K	S	L	H	Y	235
ATT	CCA	GGC	TTT	CCT	GAT	CGG	AAA	AGA	TTT	GGG	GCA	GGA	ACA	TTA	AAG	AGC	CTT	CAT	TAT	705
D	*																			237
GAC	TGA																			711
←SEQ ID NO:3↑																				
ATTACACTCATCCTTGGAAAGAGTGAGCAAGCAGTGGCAGTTTTCACAGCTCATCTTGTGTGTTCAATTATTACCAT																				
CACAGCCCTTTAACAAAATCATCTTAAATGCTACCCCTCAGCCTTACCTTAAATGGAAAAATGAAAGGGAGTGACAA																				
TACGGGAGGTCCAAACTTGTCCCTGTTCTGTGTTCTTACCTTCTGTCCCTGTGTATAGATTATGTAAAAGCCTT																				
GTGTAATATGAGATGTTGTCAAAATGATGCACTGAGCAATGACAGTGTACTGCAGAGAAAATTACTCTTGCCT																				
AGAACTGGAGGGTTTTATGGGTCTGTAATTTCACACTCATGCTGAAGCTTAATTAAAGTACTTCATAAACGTAT																				
CTCCATTGTTTACCTCTTGAGGGAACGGCTTGTAAACCAGCCCTGAGTTGTCTACCCCAACCATCTGTCAATT																				
TTCAAAGATGCAAAATGGGTTATTAAATTGTCTCCACCATGTCACACACAGGAATGCCATAATAAGCAGCCCTGT																				
CTCCCTCTCTCCTTGCATAATGGCTCAGTGACTGGAAGAGGGCGGACTAATAGCCAGAGTTAAATATAAATACAAAT																				

TAATAATACATAGAGAACAGCAATACCAGAAAAAGAATTCTGGTAAAATGATGTGAAAATTGACAGCTCCCTCACT
CTTAAGGTTGCTGCTATATACAGTCTAGGTTCTGTTGGAAATAGGTAGGGTAAAATCTAAGACCTGCACAAGGGCA
GTGAGAGACATTTACAGCCTCCTCTATTGTTTTAAGGAAAGTCAACTCCTGAAATGTCCCTAGCTATAATC
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CATGAATTATTGAAC

1000 800 600 400 200 0

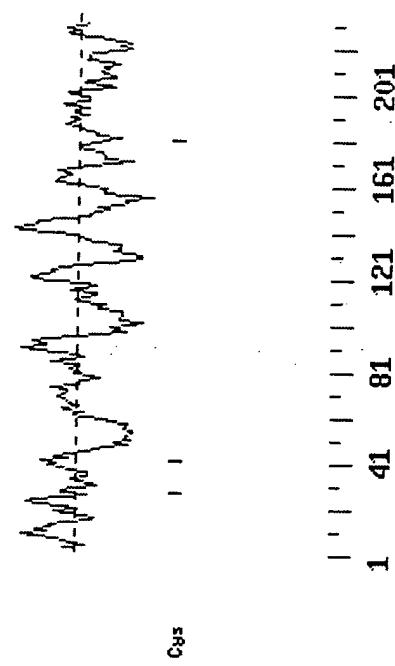


FIG. 2

*->Glgflkiflk11glwnKEmRILiLGLDnAGKTTILykLklge.ivtt SEQ ID NO:4
47324 2 -----ASLDR---VKVLVLGDSGVGKSSLVHLLCQNQvLGNP 35
iPTiGFNvEtveykN.....ikFtvWDvGGQ.....eslRP1W
+ T+G v v + + +++++++ + WDvGG ++ ++ +s R +
47324 36 SWTVGCSV-DVRVHDykegtpeektYYIELWDVGGSvgsassvKSTRAV- 83
rnYfpnTdavIfVVDSaDreRieeakeELhaLLneeeL.....
+ +++++IfV D ++ + + L + e +++ +++ ++
47324 84 --FYNSVNGIIFVHDLTNKK---SSQNLRRWSLEALNrdlvptgvln 127
.....adAp1LifANKQD1pgAmseaEi...realgLhelkgskg
++ + + + + plL+ + K D + +E+ +++ L +
47324 128 gdydqeafadNQIPLLVIGTKLDQIHETKRHEVltrTAFLAEDFNP-E-- 174
kVt1.e.gdRpWeiiggcsAvkGeGLyEGldWLsnnikkkr<-*
++ 1+ ++ R + ++Avk 1 + + + + +
47324 175 EINLdCtNPRYLAAGSSNAVK-----LSRFFDKVIEK 206

FIG. 3

*->KVLiGDsGVGKSSl1iRFTdnkFveeYipTIGvDFytktvevD... SEQ ID NO:5
47324 8 KVLVLGDSGVGKSSLVHLLCQNQVGNPSWTVGCSVDVRVHDYKegt 54
..GktvkLqIWDTAGQERFralrpa.....YYRgAqGfLLVYDITs
++ kt+ ++WD G ++ +a++ +++++ +Y +G++ V D T+
47324 55 peEKYYIELWDVGG----SVGSAssvkstravFYNSVNGIIFVHDLTN 99
rdSFenvkkWleeilr..had.....kdenvpivLVGNKC
++S +n++W e l+++ +++ +++++ +d+ +p + +G+K
47324 100 KKSSQNLRRWSLEALNrdlVptgvln 149
DLeddedlelte.gqkRvVsteeGealAkelgA.....1pFmETSA
D + e++ +V t ++ 1A++++ ++ + + ++ +++ +
47324 150 DQIH-----EtKR-HEVLTRTAF-LAEDFNPeelinldctnPRYLAAGS 190
KtntNveeaFeelareilkkvsevnvnldqpaakkkskCcil<-*
+++ F+ +++++ + +++++++ + +k+ +
47324 191 SNAVKLSRFFDKVIEKRYFLREGNQIPGFPD-RKRGAGTLK 231

FIG. 4

Query: 35 PSWTV-GCSVDRVHDYKEGTPEEK--YYIELWDXXXXXXXXXXXXXTRAVFYNSVNGI 91
P+WT S D + Y TP Y+E +D R FY +++GI
Sbjct: 69 PTWTPSSSEDSENPYMRSTPTTNILYFVEFYDLNSDWRMCRQQ---RESFYKNIDGI 125 SEQ ID
NO:6

Query: 92 IFVHDLTNKSSQNLRRWSLEALNRDLVPTGVLTNGDYDQEKFADNQIPLLVIGTKLDQ 151
+ V+++ S +L W + L + + + + + P+LV+GT LD+
Sbjct: 126 VLVYNMELSSQDSLHDWLYDPLRQICKHRHLR-----RSILKNHNAPILVVGTNLDK 179

Query: 152 IHETKRHEVLTRTAFLAEDFNPEEINLDCTNPRYLAAGSSNAVKLSRFFDKVIE-KRYF 209
+ L R +A N EE+ ++C +P+ S N KL F ++VIE K F
Sbjct: 180 L----MRRPLRRRGSIAHQLNVEEMLVNCLDPQSFVDKSRNQGKLYGFLNRVIEFKEQF 234

FIG. 5a

Query: 7 VKVLVLGDSGVGKSSLVHLLCQNQVLGNP-SWTVG---CSVDRVHDYKE 52
V++L+LGD GVGK+SL +L+ ++ P S TVG V VR+H+Y +
Sbjct: 12 VRILMLGDRGVGKTSNLNLMATTEITPTPDSRTVGEESWHVQVRLHEYSK 61 SEQ ID NO:7

FIG. 5b

Query: 121 TGVLVTNGD--YDQEKFAD-NQIPLLVIGTKLDQIHETKRHEVL--TRTAFLAEDFNPEE 175
T L T+G +D E+F Q P+LV+GTLD + E KRH + + +A+ EE
Sbjct: 19 TDNLGTDGHILFDMEFLGATQTPILVMGTKLDLLDE-KRHPKMGVKKPGGIADKCGAEE 77 SEQ ID
NO:8

Query: 176 INLDCTNPRYLAAGSSNAVKLSRFFDKVIEKRYFLR-----EGNQIPGFPDRKRGAG 228
I L+C N R LAAG+++AVKLSRFFD+VIE R LR + PDR+RFG
Sbjct: 78 IWLNCRNSRSLAAGTTDAVKLSRFFDRVIENRKALRAALAFGVSSSSNAVSPPDRRRGPT 137

Query: 229 TLK 231
+ K
Sbjct: 138 SAK 140

FIG. 6

Query: 6 RVKVLVLGDSGVGKSSLVHLLCQNQVLGNPSWTVGCSVDVRVHDYKEGTPEEKTYYIE 63
+V+VLV+GDSGVGK+SLVHL+ + + P T+GC+V V+ Y G+P + I+
Sbjct: 80 QVRVLVVGDSGVGKTSLVHLINKSSIVRPPQTIGCTVGVKHITY--GSPASSSSSIQ 135 SEQ ID NO:9

FIG. 7

Query: 8 KVLVLGDSGVGKSSLVHLL--CQNQ-----VLGNPSWTVGCSVDVRVHDYKEGT 54
K++++GDSGVGK+SL++ L +N V+ + T+G +V+ T
Sbjct: 7 KIVIIGDSGVGKTSLLNKLRTENSFTEEYDPTTRTVVDSYKSTIGVDFNVKTTIEVVDT 66 SEQ ID
NO:10

Query: 55 PEEKTYYIELWDXXXXXXXXXXXXXXTRAVFYNSVNGIIFVHDLTNKKSS-QNLRRWSLEA 113
+ K +++WD A +Y I V+D+ + +SS +N +W E
Sbjct: 67 -DGKNIKLQIWDTAGQERYRSMLTSMEA-YYRGAEADIIIVYDVSSESSFENQTKWLKEI 124

Query: 114 LNRDLVPTGVLVTNGDYDQEKFADNQIPLLIGTKLD-QI---HETKRHEVLTRTAFLAE 169
L +N E+ ++N +P++++G K D ++ E + + T A+
Sbjct: 125 LRH-----ASN-----EEASEN-VPIILVGNKADLEVPNPEEEKEEASTEEEAQ 170

Query: 170 DFNPEEINLDCTNPRYLAAGSSNAVKLSRFFDKVIEKRYFLREGNQIPGFPDRKRF 225
F EE L P + + + F +++ R L++ +I D++++
Sbjct: 171 SF-AEEKGLGVV-PFIETSAKTTGTNVVEVFQELV--REILKKKEIQEKADQEKY 222

FIG. 8